SEQUENCE LISTING

<110> BARCHFELD, Gail
DEL GIUDICE, Giuseppe
RAPPUOLI, Rino

<120> DETOXIFIED MUTANTS OF BACTERIAL ADP-RIBOSYLATING TOXINS AS PARENTERAL ADJUVANTS

<130> 2302-1393 / PP01393.002

<140> 09/044,696
<141> 1998-03-18

<160> 5

<170> PatentIn Ver. 2.0

<210> 1
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(708)

<220>
<223> Description of Artificial Sequence: wild-type Subunit A from E. coli heat labile toxin

F3

<400> 1

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aat ggc gac aga tta tac cgt gct gac tct aga ccc cca gat gaa ata   48
Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
  1               5                  10                  15

aaa cgt ttc cgg agt ctt atg ccc aga ggt aat gag tac ttc gat aga   96
Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
             20                  25                  30

gga act caa atg aat att aat ctt tat gat cac gcg aga gga aca caa   144
Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
         35                  40                  45

acc ggc ttt gtc aga tat gat gac gga tat gtt tcc act tct ctt agt   192
Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
     50                  55                  60

ttg aga agt gct cac tta gca gga cag tat ata tta tca gga tat tca   240
Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
 65                  70                  75                  80

ctt act ata tat atc gtt ata gca aat atg ttt aat gtt aat gat gta   288
Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
                 85                  90                  95

att agc gta tac agc cct cac cca tat gaa cag gag gtt tct gcg tta   336
Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
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            100                 105                 110

ggt gga ata cca tat tct cag ata tat gga tgg tat cgt gtt aat ttt   384
Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
        115                 120                 125

ggt gtg att gat gaa cga tta cat cgt aac agg gaa tat aga gac cgg   432
Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
    130                 135                 140

tat tac aga aat ctg aat ata gct ccg gca gag gat ggt tac aga tta   480
Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
145                 150                 155                 160

gca ggt ttc cca ccg gat cac caa gct tgg aga gaa gaa ccc tgg att   528
Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
                165                 170                 175

cat cat gca cca caa ggt tgt gga gat tca tca aga aca atc aca ggt   576
His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
            180                 185                 190

gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc agg   624
Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
        195                 200                 205

gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag tca   672
Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
    210                 215                 220

gag gtt gac ata tat aac aga att cgg gat gaa tta tga               711
Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
225                 230                 235
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F3

<210> 2
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: wild-type Subunit A from E. coli heat labile toxin

<400> 2

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Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
  1               5                  10                  15

Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
             20                  25                  30

Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
         35                  40                  45

Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
     50                  55                  60

Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
```

```
 65                  70                  75                  80

Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
                 85                  90                  95

Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
            100                 105                 110

Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
        115                 120                 125

Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
    130                 135                 140

Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
145                 150                 155                 160

Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
                165                 170                 175

His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
            180                 185                 190

Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
        195                 200                 205

Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
    210                 215                 220

Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
225                 230                 235
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F3

<210> 3
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(720)

<220>
<223> Description of Artificial Sequence: wild-type CT subunit A

<400> 3

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Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
  1               5                  10                  15

aag cag tca ggt ggt ctt atg cca aga gga cag agt gag tac ttt gac   96
Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
             20                  25                  30

cga ggt act caa atg aat atc aac ctt tat gat cat gca aga gga act   144
Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
         35                  40                  45
```

```
cag acg gga ttt gtt agg cac gat gat gga tat gtt tcc acc tca att   192
Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
     50                  55                  60

agt ttg aga agt gcc cac tta gtg ggt caa act ata ttg tct ggt cat   240
Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
 65                  70                  75                  80

tct act tat tat ata tat gtt ata gcc act gca ccc aac atg ttt aac   288
Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
                 85                  90                  95

gtt aat gat gta tta ggg gca tac agt cct cat cca gat gaa caa gaa   336
Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
            100                 105                 110

gtt tct gct tta ggt ggg att cca tac tcc caa ata tat gga tgg tat   384
Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
        115                 120                 125

cga gtt cat ttt ggg gtg ctt gat gaa caa tta cat cgt aat agg ggc   432
Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
    130                 135                 140

tac aga gat aga tat tac agt aac tta gat att gct cca gca gca gat   480
Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
145                 150                 155                 160

ggt tat gga ttg gca ggt ttc cct ccg gag cat aga gct tgg agg gaa   528
Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
                165                 170                 175

gag ccg tgg att cat cat gca ccg ccg ggt tgt ggg aat gct cca aga   576
Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
            180                 185                 190

tca tcg atc agt aat act tgc gat gaa aaa acc caa agt cta ggt gta   624
Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
        195                 200                 205

aaa ttc ctt gac gaa tac caa tct aaa gtt aaa aga caa ata ttt tca   672
Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
    210                 215                 220

ggc tat caa tct gat att gat aca cat aat aga att aag gat gaa tta   720
Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
225                 230                 235                 240

tga                                                               723
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F3

<210> 4
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: wild-type CT

subunit A

<400> 4

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 1               5                  10                  15

Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
            20                  25                  30

Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
        35                  40                  45

Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
    50                  55                  60

Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
65                  70                  75                  80

Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
                85                  90                  95

Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
            100                 105                 110

Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
        115                 120                 125

Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
    130                 135                 140

Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
145                 150                 155                 160

Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
                165                 170                 175

Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
            180                 185                 190

Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
        195                 200                 205

Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
    210                 215                 220

Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
225                 230                 235                 240
```

<210> 5
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: wild-type Subunit A from E. coli heat labile toxin

<400> 5

```
Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
 1               5                  10                  15

Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr Phe Asp
            20                  25                  30

Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
        35                  40                  45

Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu
    50                  55                  60

Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser Gly Tyr
65                  70                  75                  80

Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
                85                  90                  95

Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu Gln Glu
            100                 105                 110

Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
        115                 120                 125

Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
    130                 135                 140

Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
145                 150                 155                 160

Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
                165                 170                 175

Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
            180                 185                 190

Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
        195                 200                 205

Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
    210                 215                 220

Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
225                 230                 235                 240
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